

10/559986

WO 2004/113520

PCT/EP2004/006805

1/23

SEQUENCE.TXT
SEQUENCE LISTING

IAP8 Rec'd PGT/PTO 08 DEC 2005

<110> Tours Nestlé Research Center

<120> Implication Of Proteinase And Proteinase Inhibitor In Coffee Flavour

<130> Patent Proteinase and Proteinase Inhibitor Coffee

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 1543

<212> DNA

<213> Coffea canephora

<220>

<221> mRNA

<222> (1)..(1543)

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<221> CDS

<222> (122)..(1315)

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CONFIRMATION COPY

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Tyr	Glu	Lys	Thr	Tyr	Ser	Thr	His	Glu	Glu	Tyr	Val	His	Arg	Leu	Gly		
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Pro	Ser	Ala	Ile	His	Gly	Val	Thr	Gln	Phe	Ser	Asp	Leu	Thr	Glu	Glu		
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SEQUENCE.TXT

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290 295 300

ccg ctt gct att gga ttg aat gcg gta ttc atg caa act tac atc ggg    1081
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305 310 315

ggt gtg tca tgt cct ctt att tgt gac aaa aag agg atc aac cat ggt    1129
Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly
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385 390 395

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<212> PRT

<213> Coffea canephora

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SEQUENCE.TXT

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Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp
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gag gat gtg aag agc aac aaa gaa gtt caa gaa ctt ggg gaa tat tgt	45	55	255
Glu Asp Val Lys Ser Asn Lys Glu Val Gln Glu Gly Glu Tyr Cys			
gtt tct gag tac aac aag agt ttg cgg aag aag aac aac gaa agt ggt	60	70	303
Val Ser Glu Tyr Asn Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly			
gct cct ata atc ttc aca tct gtg gtg glu gct gag aag cag gtg gtt	80	85	351
Ala Pro Ile Ile Phe Thr Ser Val Val Glu Ala Glu Lys Gln Val Val			
gct ggg atc aaa tat tat ctc aag att aag gcc acc act tct tct ggg	95	100	399
Ala Gly Ile Lys Tyr Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly			
gtt ccc aag gtt tac gat gcc att gtg gtg gtt cgg cct tgg gtt cat	110	115	447
Val Pro Lys Val Tyr Asp Ala Ile Val Val Val Arg Pro Trp Val His			
act aag cca agg cag ttg ctc aac ttc tcc cct tcc cct gcc act aaa	125	130	495
Thr Lys Pro Arg Gln Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys			
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CONFIRMATION COPY

SEQUENCE.TXT

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Thr ser Val Val Glu Ala Glu Lys Gln Val Val Ala Gly Ile Lys Tyr
 85 90 95

Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly Val Pro Lys Val Tyr
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1 5 10

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15 20 25

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Ser Leu Gly Ile Asp Leu Thr Leu Tyr Asp Met Lys Ala Ser Ser Thr
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Gly Arg Leu Val Thr Cys Asp Gln Asp Phe Cys Leu Ser Ala Phe Asn
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gcc cca gcc tct gat tgc aag gtt ggt aac ccc tgt gca tat tct gtt 759
Ala Pro Ala Ser Asp Cys Lys Val Gly Asn Pro Cys Ala Tyr Ser Val
95 100 105

act tac gga gac ggg agc tca acc ggc gga tat ttt gtc aga gac tat 807
Thr Tyr Gly Asp Gly Ser Ser Thr Gly Gly Tyr Phe Val Arg Asp Tyr
110 115 120

gca aaa ctt aat caa ctg acg gga aat ctt caa acc ata ccc atg aat 855
Ala Lys Leu Asn Gln Leu Thr Gly Asn Leu Gln Thr Ile Pro Met Asn
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Gly Ser Ile Val Phe Gly Cys Ser Ser Gln Gln Ser Gly Glu Leu Gly
140 145 150 155

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Ser Ser Thr Glu Ala Val Asp Gly Ile Ile Gly Phe Gly Gln Ala Asn
160 165 170

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Ser Ser Ile Ile Ser Gln Leu Ala Ser Ala Gly Lys Val Lys Lys Ile
175 180 185

ttt tca cat tgc ttg gat ggt atc aat gga gga ggc ata ttt gct att 1047
Phe Ser His Cys Leu Asp Gly Ile Asn Gly Gly Gly Ile Phe Ala Ile
190 195 200

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Val	Gly	Ser	His	Ile	Ile	Ser	Ser	Ala	Arg	Gly	Leu	Asn	Ala	Gly	Lys
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Leu	Ile	Pro													
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10/23

SEQUENCE.TXT

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35 40 45

Cys Ala Gly Cys Val Arg Cys Pro Lys Lys Ser Ser Leu Gly Ile Asp
50 55 60

Leu Thr Leu Tyr Asp Met Lys Ala Ser Ser Thr Gly Arg Leu Val Thr
65 70 75 80

Cys Asp Gln Asp Phe Cys Leu Ser Ala Phe Asn Ala Pro Ala Ser Asp
85 90 95

Cys Lys Val Gly Asn Pro Cys Ala Tyr Ser Val Thr Tyr Gly Asp Gly
100 105 110

Ser Ser Thr Gly Gly Tyr Phe Val Arg Asp Tyr Ala Lys Leu Asn Gln
115 120 125

Leu Thr Gly Asn Leu Gln Thr Ile Pro Met Asn Gly Ser Ile Val Phe
130 135 140

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SEQUENCE.TXT

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Val Asp Gly Ile Ile Gly Phe Gly Gln Ala Asn Ser Ser Ile Ile Ser
 165 170 175

Gln Leu Ala Ser Ala Gly Lys Val Lys Lys Ile Phe Ser His Cys Leu
 180 185 190

Asp Gly Ile Asn Gly Gly Gly Ile Phe Ala Ile Gly Gln Val Val Gln
 195 200 205

Pro Lys Leu Lys Thr Thr Pro Leu Val Pro Asn Glu Ala His Tyr Asn
 210 215 220

Val Val Leu Asn Ala Ile Glu Val Gly Gly Asp Val Leu Asn Leu Pro
 225 230 235 240

Ser Asp Val Leu Gly Gly Gly Ser Gly Ser Gly Thr Ile Ile Asp Ser
 245 250 255

Gly Thr Thr Leu Ala Tyr Leu Pro Asp Asp Val Tyr Thr Pro Leu Met
 260 265 270

Glu Lys Ile Thr Ala Ser Gln Ser Asn Leu Lys Ile His Ile Val Glu
 275 280 285

Asn Gln Phe Lys Cys Phe Val Tyr Ser Gly Asn Val Asp Asp Gly Phe
 290 295 300

Pro Val Val Ser Phe His Phe Glu Asp Ser Leu Ser Leu Thr Val Tyr
 305 310 315 320

Pro His Glu Tyr Leu Phe Asp Leu His Asp Asp Gln Trp Cys Ile Gly
 325 330 335

Trp Gln Asn Lys Gly Met Gln Thr Arg Asp Gly Arg Glu Val Thr Leu
 340 345 350

Leu Gly Asp Leu Val Leu Ala Asn Lys Leu Val Ser Tyr Asp Leu Glu
 355 360 365

Asn Gln Thr Ile Gly Trp Ala Glu Tyr Asn Cys Ser Ser Ser Ile Lys
 370 375 380

Leu Arg Asp Glu Lys Ser Gly Asn Val Tyr Ala Val Gly Ser His Ile
 385 390 395 400

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Ile Ser Ser Ala Arg Gly Leu Asn Ala Gly Lys Ala Leu Arg Phe Leu
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Leu Leu Ile Ile Thr Ser Leu Leu His Ala Leu Leu Ile Pro
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<210> 7

<211> 1819

<212> DNA

<213> Coffea canephora

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<222> (79)..(1602)

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 Met Glu Arg Arg Tyr Leu Trp Ala Ala Phe Val
 1 5 10
 tta ggg gcg att gtg tgt tct cta ttt cct ctt cct tct gaa gga tta 159
 Leu Gly Ala Ile Val Cys Ser Leu Phe Pro Leu Pro Ser Glu Gly Leu
 15 20 25
 aag cga att agc ctg aaa aaa aaa ccc tta gat att caa agc ata aga 207
 Lys Arg Ile Ser Leu Lys Lys Lys Pro Leu Asp Ile Gln Ser Ile Arg
 30 35 40
 gct gcc aaa tta gct cat ctg gag agc aca cat ggc gct ggt agg aaa 255
 Ala Ala Lys Leu Ala His Leu Glu Ser Thr His Gly Ala Gly Arg Lys
 45 50 55
 gag atg gac aac aat tta ggc agt tcc aat gag gac ata ttg cct tta 303
 Glu Met Asp Asn Asn Leu Gly Ser Ser Asn Glu Asp Ile Leu Pro Leu
 60 65 70 75
 aag aat tac ctg gat gcc cag tac tat gga gag att gga att ggt act 351

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Lys	Asn	Tyr	Leu	Asp	Ala	Gln	Tyr	Tyr	Gly	Glu	Ile	Gly	Ile	Gly	Thr		
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cca	cct	cag	aag	ttc	aca	ggt	ata	ttt	gat	aca	ggc	agt	tcc	aac	ctc		399
Pro	Pro	Gln	Lys	Phe	Thr	Val	Ile	Phe	Asp	Thr	Gly	Ser	Ser	Asn	Leu		
			95					100					105				
tgg	gtg	cca	tcg	gca	aaa	tgt	tac	ttc	tct	att	gcc	tgc	tgg	ctc	cac		447
Trp	Val	Pro	Ser	Ala	Lys	Cys	Tyr	Phe	Ser	Ile	Ala	Cys	Trp	Leu	His		
		110					115					120					
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Ser	Lys	Tyr	Lys	Ala	Lys	Lys	Ser	Ser	Thr	Tyr	Thr	Ala	Ile	Gly	Lys		
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Ser	Cys	Ser	Ile	Arg	Tyr	Gly	Ser	Gly	Ser	Ile	Ser	Gly	Phe	Ser	Ser		
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cag	gat	aac	ggt	gaa	ggt	ggt	gat	ctt	ggt	gtc	aaa	gat	caa	ggt	ttt		591
Gln	Asp	Asn	Val	Glu	Val	Gly	Asp	Leu	Val	Val	Lys	Asp	Gln	Val	Phe		
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att	gaa	gct	tca	cga	gaa	gga	agt	ctt	aca	ttt	gta	att	gcc	aag	ttt		639
Ile	Glu	Ala	Ser	Arg	Glu	Gly	Ser	Leu	Thr	Phe	Val	Ile	Ala	Lys	Phe		
			175					180					185				
gac	ggg	ata	ctt	ggc	ctt	gga	ttc	cag	gag	atc	gct	ggt	gat	aac	atg		687
Asp	Gly	Ile	Leu	Gly	Leu	Gly	Phe	Gln	Glu	Ile	Ala	Val	Asp	Asn	Met		
		190					195					200					
gtg	ccg	gtc	tgg	tat	aat	atg	gtg	gac	caa	ggt	ctc	gtg	gat	gag	caa		735
Val	Pro	Val	Trp	Tyr	Asn	Met	Val	Asp	Gln	Gly	Leu	Val	Asp	Glu	Gln		
	205					210					215						
gta	ttc	tct	ttc	tgg	ctt	aac	cgc	gac	cca	aat	gct	gaa	gac	gga	ggt		783
Val	Phe	Ser	Phe	Trp	Leu	Asn	Arg	Asp	Pro	Asn	Ala	Glu	Asp	Gly	Gly		
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gag	ctg	gtc	ttt	ggt	ggt	gta	gat	aca	aat	cac	ttc	aag	gga	aag	cat		831
Glu	Leu	Val	Phe	Gly	Gly	Val	Asp	Thr	Asn	His	Phe	Lys	Gly	Lys	His		
				240					245					250			
aca	tat	ggt	cct	gta	act	cag	aag	gga	tac	tgg	caa	ttt	aaa	atg	gga		879
Thr	Tyr	Val	Pro	Val	Thr	Gln	Lys	Gly	Tyr	Trp	Gln	Phe	Lys	Met	Gly		
			255					260					265				
gat	ttt	ctc	att	ggg	aac	gtc	tca	aca	ggc	ttt	tgt	gaa	gga	ggt	tgt		927
Asp	Phe	Leu	Ile	Gly	Asn	Val	Ser	Thr	Gly	Phe	Cys	Glu	Gly	Gly	Cys		
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gct	gct	att	gtg	gac	tct	gga	aca	tcg	ttg	ctc	gct	ggt	cca	act	act		975
Ala	Ala	Ile	Val	Asp	Ser	Gly	Thr	Ser	Leu	Leu	Ala	Gly	Pro	Thr	Thr		
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gtt	gtg	act	caa	att	aat	cat	gcc	att	gga	gct	gaa	gga	gta	gtt	agc		1023
Val	Val	Thr	Gln	Ile	Asn	His	Ala	Ile	Gly	Ala	Glu	Gly	Val	Val	Ser		
					305				310						315		
act	gaa	tgt	aaa	gaa	att	gtt	tca	cag	tat	ggt	gaa	ctg	att	tgg	gat		1071
Thr	Glu	Cys	Lys	Glu	Ile	Val	Ser	Gln	Tyr	Gly	Glu	Leu	Ile	Trp	Asp		
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ctc ctc gta tca ggg gta cta ccc gac aga gtt tgt aaa caa gct ggt	1119
Leu Leu Val Ser Gly Val Leu Pro Asp Arg Val Cys Lys Gln Ala Gly	
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tta tgt ccc ctt cgt ggt gct cag cat gag aat gct tat atc aag tca	1167
Leu Cys Pro Leu Arg Gly Ala Gln His Glu Asn Ala Tyr Ile Lys Ser	
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gtc gtc gac gag gag aac aag gag gaa gct tct gtt ggt gaa tcc ccg	1215
Val Val Asp Glu Glu Asn Lys Glu Glu Ala Ser Val Gly Glu Ser Pro	
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	370
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atg tgt act gct tgt gaa atg gct gtt gtt tgg atg caa aac cag ctg	1263
Met Cys Thr Ala Cys Glu Met Ala Val Val Trp Met Gln Asn Gln Leu	
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	385
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aaa cag cag gga act aag gag aaa gtg ctt gca tat gtg aat cag ctt	1311
Lys Gln Gln Gly Thr Lys Glu Lys Val Leu Ala Tyr Val Asn Gln Leu	
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tgt gaa agc ata cca agt ccc atg gga gaa tcc atc att gac tgc aac	1359
Cys Glu Ser Ile Pro Ser Pro Met Gly Glu Ser Ile Ile Asp Cys Asn	
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agt tta tcc acc ctg cca aat gtt tca ttc acc atc gga ggg aaa agt	1407
Ser Leu Ser Thr Leu Pro Asn Val Ser Phe Thr Ile Gly Gly Lys Ser	
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ttt gag ctg acc ctt aag gag tat gtt ctt cga act gga gaa ggc ttt	1455
Phe Glu Leu Thr Leu Lys Glu Tyr Val Leu Arg Thr Gly Glu Gly Phe	
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gct gaa gtc tgc atc agt gga ttc atg gct atg gat gtg ccg ccg cct	1503
Ala Glu Val Cys Ile Ser Gly Phe Met Ala Met Asp Val Pro Pro Pro	
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	475
cgt ggt ccc atc tgg gtt ctg gga gat gtg ttc atg gga gtg tac cac	1551
Arg Gly Pro Ile Trp Val Leu Gly Asp Val Phe Met Gly Val Tyr His	
	480
	485
	490
acc gtg ttt gat tat ggt aat ctc cgg atg ggt ttc gca aga gct gct	1599
Thr Val Phe Asp Tyr Gly Asn Leu Arg Met Gly Phe Ala Arg Ala Ala	
	495
	500
	505
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aagacatgta gtagcttgta aattaggatt taattatgct tggctggttt atgggtggtg	1712
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<210> 8

<211> 507

<212> PRT

<213> Coffea canephora

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15/23

SEQUENCE.TXT

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Cys Ser Leu Phe Pro Leu Pro Ser Glu Gly Leu Lys Arg Ile Ser Leu
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Lys Lys Lys Pro Leu Asp Ile Gln Ser Ile Arg Ala Ala Lys Leu Ala
 35 40 45

His Leu Glu Ser Thr His Gly Ala Gly Arg Lys Glu Met Asp Asn Asn
 50 55 60

Leu Gly Ser Ser Asn Glu Asp Ile Leu Pro Leu Lys Asn Tyr Leu Asp
 65 70 75 80

Ala Gln Tyr Tyr Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Lys Phe
 85 90 95

Thr Val Ile Phe Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ala
 100 105 110

Lys Cys Tyr Phe Ser Ile Ala Cys Trp Leu His Ser Lys Tyr Lys Ala
 115 120 125

Lys Lys Ser Ser Thr Tyr Thr Ala Ile Gly Lys Ser Cys Ser Ile Arg
 130 135 140

Tyr Gly Ser Gly Ser Ile Ser Gly Phe Ser Ser Gln Asp Asn Val Glu
 145 150 155 160

Val Gly Asp Leu Val Val Lys Asp Gln Val Phe Ile Glu Ala Ser Arg
 165 170 175

Glu Gly Ser Leu Thr Phe Val Ile Ala Lys Phe Asp Gly Ile Leu Gly
 180 185 190

Leu Gly Phe Gln Glu Ile Ala Val Asp Asn Met Val Pro Val Trp Tyr
 195 200 205

Asn Met Val Asp Gln Gly Leu Val Asp Glu Gln Val Phe Ser Phe Trp
 210 215 220

Leu Asn Arg Asp Pro Asn Ala Glu Asp Gly Gly Glu Leu Val Phe Gly
 225 230 235 240

Gly Val Asp Thr Asn His Phe Lys Gly Lys His Thr Tyr Val Pro Val

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Ser	Gly 290	Thr	Ser	Leu	Leu	Ala 295	Gly	Pro	Thr	Thr	Val 300	Val	Thr	Gln	Ile
Asn 305	His	Ala	Ile	Gly	Ala 310	Glu	Gly	Val	Val	Ser 315	Thr	Glu	Cys	Lys	Glu 320
Ile	Val	Ser	Gln	Tyr 325	Gly	Glu	Leu	Ile	Trp 330	Asp	Leu	Leu	Val	Ser 335	Gly
Val	Leu	Pro	Asp 340	Arg	Val	Cys	Lys	Gln 345	Ala	Gly	Leu	Cys	Pro 350	Leu	Arg
Gly	Ala	Gln 355	His	Glu	Asn	Ala	Tyr 360	Ile	Lys	Ser	Val	Val 365	Asp	Glu	Glu
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Glu 385	Met	Ala	Val	Val	Trp 390	Met	Gln	Asn	Gln	Leu 395	Lys	Gln	Gln	Gly	Thr 400
Lys	Glu	Lys	Val	Leu 405	Ala	Tyr	Val	Asn	Gln 410	Leu	Cys	Glu	Ser	Ile 415	Pro
Ser	Pro	Met	Gly 420	Glu	Ser	Ile	Ile	Asp 425	Cys	Asn	Ser	Leu	Ser 430	Thr	Leu
Pro	Asn	Val 435	Ser	Phe	Thr	Ile	Gly 440	Gly	Lys	Ser	Phe	Glu 445	Leu	Thr	Leu
Lys	Glu 450	Tyr	Val	Leu	Arg	Thr 455	Gly	Glu	Gly	Phe	Ala 460	Glu	Val	Cys	Ile
Ser 465	Gly	Phe	Met	Ala	Met 470	Asp	Val	Pro	Pro	Pro 475	Arg	Gly	Pro	Ile	Trp 480
Val	Leu	Gly	Asp	Val 485	Phe	Met	Gly	Val	Tyr 490	His	Thr	Val	Phe	Asp 495	Tyr

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Gly Asn Leu Arg Met Gly Phe Ala Arg Ala Ala
 500 505

<210> 9
 <211> 726
 <212> DNA
 <213> Coffea canephora

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cagtgaatct aagggcaatg agaacagcct tgaaattgag agcctggcta agtttgctgt    180
ggatgattac aacaagaaac agaatgccct tttggaattt cagaagggtga tcaacagtaa    240
agagcagggt gttgctggta ccgtgtacta tctgaccatt gaggtgaaag atgggaatga    300
gaagaagctt tatgaggcca aagtttggtt gaagccatgg ttgaacttca aggaggttca    360
agaattcaag cctgctgctg gtgatactag tgcctaaatt tgcttcttaa caatgcgcta    420
ttgcctatct gcctagtaga aataaagcta acgcgtaaat gtctttcagt tggaaagatt    480
ggagtttcaa acatgcttag tttgtatatg ctataactcg taatattaac atgttagtaa    540
catgttatct tatgttgat agatgttaag accaacataa tcttcgctga tgttcggttc    600
gatgtgatct gatcctgtgg tttttatacc actctggctt gagtatcatt acccttagtc    660
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aaaaaa                                           726
  
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<210> 10
 <211> 98
 <212> PRT
 <213> Coffea canephora

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Leu Glu Ile Glu Ser Leu Ala Lys Phe Ala Val Asp Asp Tyr Asn Lys
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Lys Gln Asn Ala Leu Leu Glu Phe Gln Lys Val Ile Asn Ser Lys Glu
  
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SEQUENCE.TXT

35

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45

Gln Val Val Ala Gly Thr Val Tyr Tyr Leu Thr Ile Glu Val Lys Asp
 50 55 60

Gly Asn Glu Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp
 65 70 75 80

Leu Asn Phe Lys Glu Val Gln Glu Phe Lys Pro Ala Ala Gly Asp Thr
 85 90 95

Ser Ala

<210> 11

<211> 688

<212> DNA

<213> Coffea canephora

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 ccaccctggc agctatctgt cttttctccg acgtcccttc cgcggctttg ggtggctgcc 180
 ccaaagatgc cttagtcggc gggtggagta aggctgacct caaggacca gaggtgctag 240
 agaacggaaa atttgccata gatgagcaca acaaggaggc cggtagcaag ttggagtta 300
 aaactgtggt ggaggcgag aagcaagtgg tggccggcac aaattacaag attgtgataa 360
 aggcattgga tggcactgct tcaaattctgt acgaggccat tgtttggtc aagccctggc 420
 tcaaattcaa gaagcttact tccttcagga aacttcctg atcagattta aggggatgta 480
 ataagcatgt gcatttcttg cttaaaactg tggcatgaga ggtgtatgta taatcatctg 540
 tatttcttgc ttaaaactgt ggtatgacta tgagagatgt ttgaagtgta ctgtactaca 600
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<211> 124

<212> PRT

<213> Coffea canephora

SEQUENCE.TXT

<400> 12

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Ile Cys Leu Phe Ser Asp Val Pro Ser Ala Ala Leu Gly Gly Arg Pro
 20 25 30

Lys Asp Ala Leu Val Gly Gly Trp Ser Lys Ala Asp Pro Lys Asp Pro
 35 40 45

Glu Val Leu Glu Asn Gly Lys Phe Ala Ile Asp Glu His Asn Lys Glu
 50 55 60

Ala Gly Thr Lys Leu Glu Phe Lys Thr Val Val Glu Ala Gln Lys Gln
 65 70 75 80

Val Val Ala Gly Thr Asn Tyr Lys Ile Val Ile Lys Ala Leu Asp Gly
 85 90 95

Thr Ala Ser Asn Leu Tyr Glu Ala Ile Val Trp Val Lys Pro Trp Leu
 100 105 110

Lys Phe Lys Lys Leu Thr Ser Phe Arg Lys Leu Pro
 115 120

<210> 13

<211> 697

<212> DNA

<213> coffea canephora

<400> 13

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 cagaaaaaca tgggtgggtgg tgggtctaagc tctactgttc ctccctgatc gtcaaccgctc 180
 aacccgaaag accctcacgt gattcagatc gcacaatttg cagttgcaaa ctacaacgcg 240
 aaggccggga ccactgtggt ttggctgaat gtggaatatg gcttctggtg gattgacgat 300
 gacacttact acatgcttgc cattaaaact caggatctta cgggcacaca ttgcgacgta 360
 gcattggttc gtgaaatatc ggagagcaat ggtacttata gcctcaaatg gtacaatcat 420
 aacaataagt gaccacgcac tactcttgat cagctgagga tcaatgactt taattatata 480

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SEQUENCE.TXT

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<210> 14

<211> 119

<212> PRT

<213> Coffea canephora

<400> 14

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Gln Lys Asn Met Val Gly Gly Gly Leu Ser Ser Thr Val Pro Pro Arg
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Ser Ser Thr Val Asn Pro Lys Asp Pro His Val Ile Gln Ile Ala Gln
 35 40 45

Phe Ala Val Ala Asn Tyr Asn Ala Lys Ala Gly Thr Thr Val Val Trp
 50 55 60

Leu Asn Val Glu Tyr Gly Phe Trp Trp Ile Asp Asp Asp Thr Tyr Tyr
 65 70 75 80

Met Leu Ala Ile Lys Thr Gln Asp Leu Thr Gly Thr His Cys Asp Val
 85 90 95

Ala Leu Val Arg Glu Ile Ser Glu Ser Asn Gly Thr Tyr Ser Leu Lys
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Trp Tyr Asn His Asn Asn Lys
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<210> 15

<211> 1367

<212> DNA

<213> Coffea canephora

SEQUENCE.TXT

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ttgccgttgt attggctgtg atcttagtgg cggctatgag catggagatc acagaaagag    180
atttggcttc tgaggaaagc ttgtgggact tgtacgaaag atggaggagc catcatactg    240
tttctcgaga cctttctgag aaacgaaagc gctttaatgt tttcaaggca aatgtccatc    300
acattcaciaa ggtgaaccag aaggacaagc cttacaagct gaaactcaac agtttcgctg    360
atatgaccaa ccacgagttc agggaaattct acagttctaa ggtgaaacat taccggatgc    420
tccacggcag tcgtgctaata actggattta tgcattggga gactgaaagt ttgccagcct    480
ccgttgattg gagaaagcaa ggagccgtga ctggcgtaa gaatcaaggc aaatgtggta    540
gctgttgggc attttcaact gtggttggag tcgagggaaat caacaaaatc aaaacaggcc    600
aattagtttc tctgtccgag caagaacttg ttgactgtga aacggacaat gaaggatgca    660
acggaggact catggaaaat gcatacgagt ttattaagaa aagtggggga ataacaactg    720
agaggctata tccctacaag gcaagagatg gcagctgtga ttcgtcaaag atgaatgccc    780
ctgctgtgac tattgatggg catgaaatgg taccgcgaaa cgatgagaat gccttgatga    840
aagctgttgc taaccagcct gtatcagtag ctatagatgc gtctggctct gacatgcaat    900
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cggtcgtcgg ctacgggact gctcttgacg gtactaaata ctggatagtg aagaactcat   1020
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aaggcggagt ttgtgggata gcaatggagg cctcctatcc acttaaattg tcctcccaca   1140
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tatatatata tttcagtaga ttcattgaat tttagttaca gactacgagc ttctgaagac   1260
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<210> 16

<211> 359

<212> PRT

<213> Coffea canephora

<400> 16

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SEQUENCE.TXT

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 Glu Glu Ser Leu Trp Asp Leu Tyr Glu Arg Trp Arg Ser His His Thr
 35 40 45
 Val Ser Arg Asp Leu Ser Glu Lys Arg Lys Arg Phe Asn Val Phe Lys
 50 55 60
 Ala Asn Val His His Ile His Lys Val Asn Gln Lys Asp Lys Pro Tyr
 65 70 75 80
 Lys Leu Lys Leu Asn Ser Phe Ala Asp Met Thr Asn His Glu Phe Arg
 85 90 95
 Glu Phe Tyr Ser Ser Lys Val Lys His Tyr Arg Met Leu His Gly Ser
 100 105 110
 Arg Ala Asn Thr Gly Phe Met His Gly Lys Thr Glu Ser Leu Pro Ala
 115 120 125
 Ser Val Asp Trp Arg Lys Gln Gly Ala Val Thr Gly Val Lys Asn Gln
 130 135 140
 Gly Lys Cys Gly Ser Cys Trp Ala Phe Ser Thr Val Val Gly Val Glu
 145 150 155 160
 Gly Ile Asn Lys Ile Lys Thr Gly Gln Leu Val Ser Leu Ser Glu Gln
 165 170 175
 Glu Leu Val Asp Cys Glu Thr Asp Asn Glu Gly Cys Asn Gly Gly Leu
 180 185 190
 Met Glu Asn Ala Tyr Glu Phe Ile Lys Lys Ser Gly Gly Ile Thr Thr
 195 200 205
 Glu Arg Leu Tyr Pro Tyr Lys Ala Arg Asp Gly Ser Cys Asp Ser Ser
 210 215 220
 Lys Met Asn Ala Pro Ala Val Thr Ile Asp Gly His Glu Met Val Pro
 225 230 235 240
 Ala Asn Asp Glu Asn Ala Leu Met Lys Ala Val Ala Asn Gln Pro Val
 245 250 255
 Ser Val Ala Ile Asp Ala Ser Gly Ser Asp Met Gln Phe Tyr Ser Glu
 260 265 270

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SEQUENCE.TXT

Gly Val Tyr Ala Gly Asp Ser Cys Gly Asn Glu Leu Asp His Gly Val
275 280 285

Ala Val Val Gly Tyr Gly Thr Ala Leu Asp Gly Thr Lys Tyr Trp Ile
290 295 300

Val Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Gln Gly Tyr Ile Arg
305 310 315 320

Met Gln Arg Gly Val Asp Ala Ala Glu Gly Gly Val Cys Gly Ile Ala
325 330 335

Met Glu Ala Ser Tyr Pro Leu Lys Leu Ser Ser His Asn Pro Lys Pro
340 345 350

Ser Pro Pro Lys Asp Asp Leu
355

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